SEQUENCE LISTING

- (1) GENERAL INFORMATION:
 - (i) APPLICANT: Huse, William D. Glaser, Scott M.
 - (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use
 - (iii) NUMBER OF SEQUENCES: 100
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Campbell & Flores LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 92122
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/016,061
 - (B) FILING DATE: 30-JAN-1998
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/791,391
 (B) FILING DATE: 30-JAN-1997
 - (viii) ATTORNEY/AGENT INFORMATION:

 - (A) NAME: Campbell, Cathryn A.(B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-IX 2965
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (619) 535-9001 (B) TELEFAX: (619) 535-8949
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..351
 - . (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10

TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val 50 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC

102

CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65. 70 75 80

CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

85 90 95

GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA 336 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr 100 105 110

GTG ACT GTT TCT AGT Val Thr Val Ser Ser 115

351

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45

Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val 50 60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr 100 105 110

Val Thr Val Ser Ser 115

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG Glu 1	ATT Ile	GTG Val	CTA Leu	ACT Thr 5	CAG Gln	TCT Ser	CCA Pro	GCC Ala	ACC Thr 10	CTG Leu	TCT Ser	CTC Leu	AGC Ser	CCA Pro 15	GGA Gly	48
GAA Glu	AGG Arg	GCG Ala	ACT Thr 20	CTT Leu	TCC Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His	96
CTA Leu	CAC His	TGG Trp 35	TAT Tyr	CAA Gln	CAA Gln	AGG Arg	CCT Pro 40	GGT Gly	CAA Gln	GCC Ala	CCA Pro	AGG Arg 45	CTT Leu	CTC Leu	ATC Ile	144
AAG Lys	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	GCC Ala 60	AGG Arg	TTC Phe	AGT Ser	GGC Gly	192
AGT Ser 65	GGA Gly	TCA Ser	GGG Gly	ACA Thr	GAT Asp 70	TTC Phe	ACC Thr	CTC Leu	ACT Thr	ATC Ile 75	TCC Ser	AGT Ser	CTG Leu	GAG Glu	CCT Pro 80	240
GAA Glu	GAT Asp	TTT Phe	GCA Ala	GTC Val 85	TAT Tyr	TAC Tyr	TGT Cys	CAA Gln	CAG Gln 90	AGT Ser	GGC Gly	AGC Ser	TGG Trp	CCT Pro 95	CAC His	288

321

(2) INFORMATION FOR SEQ ID NO:4:

100

(i) SEQUENCE CHARACTERISTICS:

ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

- (A) LENGTH: 107 amino acids (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 10

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro 65 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His 90 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 351 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG 48 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT 96 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr 20 25 GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val GCA AAA GTT AGT AGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG 192 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val 50 CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC 240 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT 288 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys 90 GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu 336 GTC ACT GTC TCT GCA Val Thr Val Ser Ala 351

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

		(xi)	SEQ	JENCI	E DES	CRI	PTIO	N: S	EQ II	ои с	:6:					
	u Vai	l Gl	n Lei	ı Va]		ı Sei	r Gl	y Gl	y Gly		u Va	l Ly	s Pr	0 Gl	y Arg 5	
Se	r Lei	ı Arg	g Let 20		Cys	s Ala	a Ala	a Se:		Ph	e Al	a Ph	e Se	_	r Tyr	
Ası) Met	: Se:		Val	Arg	Glr	1 Ile 40		Glu	ı Ly:	s Ar	g Le		ı Tr	o Val	
Ala	Lys 50	Val	l Ser	Ser	Gly	Gl _y 55	Gly	y Sei	Thr	ту	r Ty:		u Ası	o Thi	val	
Glr 69	ı Gly	Arg	y Phe	Thr	Ile 70		Arg	J Asp	Asn	1 Ala 75		a Ası	n Thi	r Lei	1 Tyr 80	
Leu	ı Gln	Met	Ser	Ser 85		Asn	Ser	Glu	Asp 90		. Ala	a Mei	туі	Tyr 95	Cys	
Ala	Arg	His	Asn 100		Gly	Ser	Phe	105		Tr	Gly	/ Glr	1 Gly		Leu	
Val	Thr	Val 115		Ala												
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 7	:								
		(() FE. ()	B) T C) S D) T ATUR: A) N. B) L	AME/1	nuc DEDNI DGY: KEY:	leic ESS: lin CDS	aci bot ear 321	d h								
CAT				CE DE								ama			~~-	
Asp 1	Ile	Val	Leu	ACT Thr 5	Gln	Ser	Pro	Ala	Thr 10	Leu	Ser	Val	Thr	Pro 15	GGA	48
GAT Asp	AGC Ser	GTC Val	AGT Ser 20	CTT Leu	TCC Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His	96
CTA Leu	CAC His	TGG Trp 35	TAT Tyr	CAA Gln	CAA Gln	AAA Lys	TCA Ser 40	CAT His	GAG Glu	TCT Ser	CCA Pro	AGG Arg 45	CTT Leu	CTC Leu	ATC Ile	144
AAG Lys	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	TCC Ser 60	AGG Arg	TTC Phe	AGT Ser	GGC Gly	192
AGT Ser 65	GGA Gly	TCA Ser	GGG Gly	ACA Thr	GAT Asp 70	TTC Phe	GCT Ala	CTC Leu	AGT Ser	ATC Ile 75	AAC Asn	AGT Ser	GTG Val	GAG Glu	ACT Thr 80	240
GAA Glu	GAT Asp	TTT Phe	GGA Gly	ATG Met 85	TAT Tyr	TTC Phe	TGT Cys	CAA Gln	CAG Gln 90	AGT Ser	GGC Gly	AGC Ser	TGG Trp	CCT Pro 95	CAC His	288

ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG

										100
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	Lys
(2)	INFO	ORMAT	CION	FOR	SEQ	ID	NO:8:	:		

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly

Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly

Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGGTGCAGC TGGTGGAGTC TGGGGGAGGC GTTGTGCAGC CTGGAAGGTC CCTGAGACTC 60 TCCTGTGCAG CCTCTGGATT CACC 84

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AACTTTTGCG ACCCACTCCA GACCCTTGCC CGGAGCCTGG CGAACCCAAG ACATGTCATA 60 GCTACTGAAG GTGAATCCAG AGGC 84

107	
(2) INFORMATION FOR SEQ ID NO:11:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:	
TGGGTCGCAA AAGTTAGTAG TGGTGGTGGT AGCACCTACT ATTTAGACAC TGTGCAGGGC	60
CGATTCACCA TCTCCAGAGA CAATAGT	87
(2) INFORMATION FOR SEQ ID NO:12:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
TGCACAGTAA TACACGGCTG TGTCCTCGGC TCTCAGAGAG TTCATTTGCA GGTATAGGGT	60
GTTCTTACTA TTGTCTCTGG A	81
(2) INFORMATION FOR SEQ ID NO:13:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GTGTATTACT GTGCAAGACA TAACTACGGC AGTTTTGCTT ACTGGGGCCA AGGGACTACA	60
GTGACTGTTT CTAGT	75
(2) INFORMATION FOR SEQ ID NO:14:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT	60
CTTTCCTGCC AGGCCAGCCA AAGTATT	87
(2) INFORMATION FOR SEQ ID NO:15:	

 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	-
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GATGAGAAGC CTTGGGGCTT GACCAGGCCT TTGTTGATAC CAGTGTAGGT GGTTGCTAAT	60
ACTTTGGCTG GC	72
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
CCAAGGCTTC TCATCWASTA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT	60
GGCAGTGGAT CAGGGACAGA TTTC	84
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
·	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GCTGCCACTC TGTTGACAGW AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT	60
GAGGGTGAAA TCTGTCCCTG A	81
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	-
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG	57
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GCCCAACCAG CCATGGCCGA TATTGTGCTA ACTCAG	36
(2) INFORMATION FOR SEQ ID NO:20:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
ACAGTTGGTG CAGCATCAGC	. 20
(2) INFORMATION FOR SEQ ID NO:21:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
ACCCCTGTGG CAAAAGCCGA AGTGCAGCTG GTGGAG	36
(2) INFORMATION FOR SEQ ID NO:22:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
GATGGGGGTG TCGTTTTGGC	20
(2) INFORMATION FOR SEQ ID NO:23:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 87 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT	60
CTTTCCTGCC AGGCCAGCCA AAGTATT	87
(a) TYPEDWARTON BOD GEO TO NO.24	

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 75 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
TTAGATGAGA AGCCTTGGGG CTTGACCAGG CCTTTGTTGA TACCAGTGTA GGTGGTTGCT	6
AATACTTTGG CTGGC	79
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 84 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CCAAGGCTTC TCATCTAATA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT	60
GGCAGTGGAT CAGGGACAGA TTTC	84
(2) INFORMATION FOR SEQ ID NO:26:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GCTGCCACTC TGTTGACAGT AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT	60
GAGGGTGAAA TCTGTCCCTG A	81
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 57 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27: CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG	57
(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear 	

	(xi) SE	QUENC	E DESC	RIPT	ION:	SEÇ] ID	NO : 2	8:						
	Ту 1	r Pr	o Tyr	Asp V		ro A	sp T	yr A		er 0						
(2)	INF	ORMA	TION	FOR SE	Q ID	NO:	29:									
	(i	(, (; ()	A) LEI B) TYI C) STI	E CHAR NGTH: PE: nu RANDED POLOGY	22 b clei NESS	ase c ac : bo	pair id th	s								
	(xi) SE	QUENCI	DESC	RIPT:	ION:	SEQ	ID I	NO:2	9:						
GCT	ACTG	AAG (GCGAA1	CCAG	AG											22
(2)	INF	ORMA:	TION E	OR SE	Q ID	NO:	30:									
	(i)	(<i>I</i> (E	A) LEN B) TYE C) STR	CHAR GTH: 1 E: nuc ANDEDI OLOGY	23 ba cleio NESS:	ase p c ac: c sin	pair: id	S								
	(ix)	(A	B) LOC D) OTH	E/KEY: ATION: ER INI specif	: 11. FORMA	$\overline{13}$	J: /r	iote=	: ""N Icid	INN" othe	repr er th	eser an I	ıts a Lys."	ı cod	on	
,	(xi)	SEQ	UENCE	DESCR	RIPTI	ON:	SEQ	ID N	ro : 3 0):						
GGG	AACGA	TA N	NNGAT	GAGA A	.GC											23
(2)	INFO	RMAT	'ION F	OR SEÇ	ID	NO:3	1:									
	(i)	(A (B (C) LENG) TYP:) STR.	CHARA GTH: 3 E: nuc ANDEDN DLOGY:	21 b leic ESS:	ase aci sin	pair d	s								
	(ix)	(A		E/KEY: ATION:		321										
	(xi)	SEQ	UENCE	DESCR	IPTI	ON:	SEQ	ID N	0:31	:						
GAG Glu 1	ATT (GTG (Val 1	CTA AC Leu Th	T CAG ir Gln 5	TCT Ser	CCA Pro	GCC Ala	ACC Thr 10	CTG Leu	TCT Ser	CTC Leu	AGC Ser	CCA Pro 15	GGA Gly		48
GAA Glu	AGG (Arg /	GCG A	ACT CT Thr Le 20	T TCC u Ser	TGC Cys	CAG Gln	GCC Ala 25	AGC Ser	CAA Gln	AGT Ser	ATT Ile	AGC Ser 30	AAC Asn	CAC His		96
CTA Leu	CAC 1 His 1	rgg 1 Trp 1 35	FAT CA Fyr Gl	A CAA n Gln	AGG Arg	CCT Pro 40	GGT Gly	CAA Gln	GCC Ala	CCA Pro	AGG Arg 4'5	CTT Leu	CTC Leu	ATC Ile		144

MKK Xaa	TAT Tyr 50	CGT Arg	TCC Ser	CAG Gln	TCC Ser	ATC Ile 55	TCT Ser	GGG Gly	ATC Ile	CCC Pro	GCC Ala 60	AGG Arg	TTC Phe	AGT Ser	GGC Gly	192
AGT Ser 65	GGA Gly	TCA Ser	GGG Gly	ACA Thr	GAT Asp 70	TTC Phe	ACC Thr	CTC Leu	ACT Thr	ATC Ile 75	TCC Ser	AGT Ser	CTG Leu	GAG Glu	CCT Pro 80	240
GAA Glu	GAT Asp	TTT Phe	GCA Ala	GTC Val 85	TAT Tyr	TAC Tyr	TGT Cys	CAA Gln	CAG Gln 90	AGT Ser	GGC Gly	AGC Ser	TGG Trp	CCT Pro 95	CAC His	288
		Gly				AAG Lys										321

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile 35 40 45

Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS-
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGA TTC ACC TTC AGT AGC TAT GAC ATG TCT
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1 10

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
- Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser 5
- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGG GTC GCA AAA GTT AGT AGT GGT GGT Trp Val Ala Lys Val Ser Ser Gly Gly Gly

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Val Ala Lys Val Ser Ser Gly Gly Gly

- (2) INFORMATION FOR SEQ ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37: AGC ACC TAC TAT TTA GAC ACT GTG CAG GGC 30 Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly 5 (2) INFORMATION FOR SEQ ID NO:38: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38: Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly 5 1 (2) INFORMATION FOR SEQ ID NO:39: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both
(D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39: GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC 30 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr 1 (2) INFORMATION FOR SEQ ID NO:40: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40: Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr (2) INFORMATION FOR SEQ ID NO:41: (i) SEQUENCE CHARACTERISTICS:

(ix) FEATURE:

(A) NAME/KEY: CDS

(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear

(B) LOCATION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CAG GCC AGC CAA AGT ATT AGC AAC CAC CTA CAC TGG TAT Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr 39

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr 5

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..33
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTT CTC ATC CGT TAT CGT TCC CAG TCC ATC TCT Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser 33

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser 1.

- (2) INFORMATION FOR SEQ ID NO:45:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: both

 - (D) TOPOLOGY: linear

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(A) NAME/KEY: CDS
            (B) LOCATION: 1..27
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:
 CAA CAG AGT GGC AGC TGG CCT CAC ACG
 Gln Gln Ser Gly Ser Trp Pro His Thr
                     5
 (2) INFORMATION FOR SEQ ID NO:46:
         (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 9 amino acids (B) TYPE: amino acid
               (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:
 Gln Gln Ser Gly Ser Trp Pro His Thr
   1
                    5
 (2) INFORMATION FOR SEQ ID NO:47:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid
           (C) STRANDEDNESS: both
           (D) TOPOLOGY: linear
     (ix) FEATURE:
           (A) NAME/KEY: CDS
           (B) LOCATION: 1..30
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:
GGA ACT ACC TTC AGT AGC TAT GAC ATG TCT
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
  ī
                   5
                                        10
(2) INFORMATION FOR SEQ ID NO:48:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 10 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
(2) INFORMATION FOR SEQ ID NO:49:
     (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 30 base pairs
```

(B) TYPE: nucleic acid (C) STRANDEDNESS: both

(ix) FEATURE:

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGA TTC ACC TGG AGT AGC TAT GAC ATG TCT Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser 1

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- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - . (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGA TTC ACC TTC CTG AGC TAT GAC ATG TCT Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser 1

- (2) INFORMATION FOR SEQ ID NO:52:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
- Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser 1 5 10
- (2) INFORMATION FOR SEQ ID NO:53:

118	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 130	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
TGG GTC GCA AAA GTT AAA AGT GGT GGT GGT Trp Val Ala Lys Val Lys Ser Gly Gly 1 5 10	30
(2) INFORMATION FOR SEQ ID NO:54:	•
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	·
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	•
Trp Val Ala Lys Val Lys Ser Gly Gly Gly 1 5 10	
(2) INFORMATION FOR SEQ ID NO:55:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear 	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 130	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:	
AGC ACC TAC TAT CCT GAC ACT GTG CAG GGC Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly 1 5 10	30
(2) INFORMATION FOR SEQ ID NO:56:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: protein	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly 1 5 10

	119	
(2)	INFORMATION FOR SEQ ID NO:57:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 130	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:	
	ACC TAC TAT TTA GAC ACT GTG GAG GGC Thr Tyr Tyr Leu Asp Thr Val Glu Gly 5	3
(2)	INFORMATION FOR SEQ ID NO:58:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 10 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
Ser 1	Thr Tyr Tyr Leu Asp Thr Val Glu Gly 5 10	
(2)	INFORMATION FOR SEQ ID NO:59:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 130	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	AGA CAT AAC CAT GGC AGT TTT GCT TAC Arg His Asn His Gly Ser Phe Ala Tyr 5 10	3
(2).	INFORMATION FOR SEQ ID NO:60:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: protein

120 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60: Ala Arg His Asn His Gly Ser Phe Ala Tyr (2) INFORMATION FOR SEQ ID NO:61: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61: GCA AGA CAT AAC TAC GGC AGT TAT GCT TAC 30 Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr (2) INFORMATION FOR SEQ ID NO:62: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62: Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr (2) INFORMATION FOR SEQ ID NO:63: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS
(B) LOCATION: 1..30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63: GCA AGA CAT AAC TAC GGC AGT TTT GAT TAC 30 Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr 1 (2) INFORMATION FOR SEQ ID NO:64: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids

(B) TYPE: amino acid(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCA AGA CAT AAC TAC GGC AGT TTT TAT TAC Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr 30

- (2) INFORMATION FOR SEQ ID NO:66:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr

- (2) INFORMATION FOR SEQ ID NO:67:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCA AGA CAT AAC TAC GGC AGT TTT GCT TCT Ala Arg His Asn Tyr Gly Ser Phe Ala Ser

- (2) INFORMATION FOR SEQ ID NO:68:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Arg His Asn Tyr Gly Ser Phe Ala Ser 5

- (2) INFORMATION FOR SEQ ID NO:69:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCA AGA CAT AAC TAC GGC AGT TTT GCT ACT Ala Arg His Asn Tyr Gly Ser Phe Ala Thr 1 5

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- (2) INFORMATION FOR SEQ ID NO:70:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ala Arg His Asn Tyr Gly Ser Phe Ala Thr

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GAT Ala Arg His Asn Tyr Gly Ser Phe Ala Asp

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala Arg His Asn Tyr Gly Ser Phe Ala Asp 1 5 10

- (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GAG Ala Arg His Asn Tyr Gly Ser Phe Ala Glu 1 5 10

30

- (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1 5 10

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GCA AGA CAT AAC TAC GGC AGT TTT GCT ATG Ala Arg His Asn Tyr Gly Ser Phe Ala Met 1

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Arg His Asn Tyr Gly Ser Phe Ala Met

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GGG Ala Arg His Asn Tyr Gly Ser Phe Ala Gly

30

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Arg His Asn Tyr Gly Ser Phe Ala Gly 1 5

- (2) INFORMATION FOR SEQ ID NO:79:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both

 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GCT Ala Arg His Asn Tyr Gly Ser Phe Ala Ala

30

- (2) INFORMATION FOR SEQ ID NO:80:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Arg His Asn Tyr Gly Ser Phe Ala Ala 5

- (2) INFORMATION FOR SEQ ID NO:81:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..39
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CAG GCC AGC CAA AGT ATT AGC AAC TTT CTA CAC TGG TAT Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr 5 1 10

39

- (2) INFORMATION FOR SEQ ID NO:82:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid -
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr

- (2). INFORMATION FOR SEO ID NO:83:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTT CTC ATC CGT TAT TCT TCC CAG TCC ATC TCT Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser 5

33

- (2) INFORMATION FOR SEQ ID NO:84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser 5

- (2) INFORMATION FOR SEQ ID NO:85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..27
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CAA CAG AGT AAT AGC TGG CCT CAC ACG Gln Gln Ser Asn Ser Trp Pro His Thr 1

27

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid(D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Gln Gln Ser Asn Ser Trp Pro His Thr

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 1..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CAA CAG AGT ACT AGC TGG CCT CAC ACT Gln Gln Ser Thr Ser Trp Pro His Thr

27

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO:88:

Gln Gln Ser Thr Ser Trp Pro His Thr

- (2) INFORMATION FOR SEQ ID NO:89:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..27
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAA CAG AGT GGC AGC TGG CCT CTG ACG Gln Gln Ser Gly Ser Trp Pro Leu Thr

27

- (2) INFORMATION FOR SEQ ID NO:90:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gln Gln Ser Gly Ser Trp Pro Leu Thr 5

- (2) INFORMATION FOR SEQ ID NO:91:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

CA Gl
(2
Gli : (2)
GCA Ala 1

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(ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..27
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
   A CAG AGT GGC AGC TGG CCT CAG ACG
                                                                          27
   n Gln Ser Gly Ser Trp Pro Gln Thr
   ) INFORMATION FOR SEQ ID NO:92:
        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 9 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
       (ii) MOLECULE TYPE: protein
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
   n Gln Ser Gly Ser Trp Pro Gln Thr
                   5
   ) INFORMATION FOR SEQ ID NO:93:
      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 30 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: both
           (D) TOPOLOGY: linear
    (ix) FEATURE:
           (A) NAME/KEY: CDS
           (B) LOCATION: 1..30
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
   AGA CAT AAC CAT GGC AGT TTT GCT TCT
                                                                         30
    Arg His Asn His Gly Ser Phe Ala Ser
                  5
(2) INFORMATION FOR SEQ ID NO:94:
       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 10 amino acids
              (B) TYPE: amino acid
             (D) TOPOLOGY: linear
      (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
Ala Arg His Asn His Gly Ser Phe Ala Ser
(2) INFORMATION FOR SEQ ID NO:95:
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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both

(D)	TOPOLOGY:	linear
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- (ix) FEATURE:
 - (A) NAME/KEY: CDS (B) LOCATION: 1..30
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GCA AGA CAT AAC CAT GGC AGT TTT TAT TCT Ala Arg His Asn His Gly Ser Phe Tyr Ser

30

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ala Arg His Asn His Gly Ser Phe Tyr Ser

- (2) INFORMATION FOR SEQ ID NO:97:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:

 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCA AGA CAT AAC TAC GGC AGT TTT TAT GAG Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu 30

- (2) INFORMATION FOR SEQ ID NO:98:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu

(2) INFORMATION FOR SEQ ID NO:99:

	CHARACTERISTICS

- (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 (B) LOCATION: 1..30
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCA AGA CAT AAC TAC GGC AGT TTT TAT TCT Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser 1

- (2) INFORMATION FOR SEQ ID NO:100:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
- Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser 5